SEQUENCE LISTING

<110> Huse, William D. Watkins, Jeffry D.

<120> Tumor Specific Human Monoclonal Antibodies and Methods of Use

<130> P-IX 2947

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<170> PatentIn Ver. 2.0

<210> 1

<211> 417

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(417)

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<221> sig_peptide

<222> (1)..(57)

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Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp

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gtc ctg tcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag 96
Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
20 25 30

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc 144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
35 40 45

agt ggt tac tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg 192 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu 50 55 60

gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg 240

Glu	Trp	Ile	Gly	Glu	Ile	Asn	His	Ser	Gly	Ser	Thr	Asn	Tyr	Asn	Pro	
65					70					75					80	
tcc	ctc	aag	agt	cga	gtc	acc	ata	tca	gta	gac	acg	tcc	aag	aac	cag	288
Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	
				85					90					95		
ttc	tcc	ctg	aag	ctg	agc	tct	gtg	acc	gcc	gcg	gac	acg	gct	gtg	tat	336
Phe	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	
			100					105			_		110		_	
tac	tgt	gcg	aga	gaa	ata	gca	gct	cgt	cct	cac	cga	tac	ttt	gac	tac	384
Tyr	Cys	Ala	Arg	Glu	Ile	Ala	Ala	Arg	Pro	His	Arg	Tyr	Phe	Asp	Tyr	
_	_	115	_				120	_			_	125		-	-	
tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca						417
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Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Trp	Gly	Ala	Gly	Leu	Leu	Lys	
			20					25					30			
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Tyr	Gly	Gly	Ser	Phe	
		35					40				_	45	_			
Ser	Gly	Tyr	Tyr	Trp	Ser.	Trp	Ile	Arg	Gln	Pro	Pro	Glv	Lvs	Glv	Leu	
	50	-	-	-		55		_			60	-	•	-		
Glu	Trp	Ile	Glv	Glu	Ile	Asn	His	Ser	Glv	Ser	Thr	Asn	Tvr	Asn	Pro	
65	•		-		70					75					80	
Ser	Len	Lvs	Ser	Ara	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lvs	Asn	G] n	
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				0.5					20					ى د		
Dho	Ser	T.e.i	Luc	Len	Ser	Se~	V = 1	ሞ⊳∽	Δ1 ¬	Δl a	Λ c ~	ጥሎ∽	717	U = 1	ጥ ~	
		нен	T V D	ᅩ┖	OCT.	∩ Œ T	vа⊥	TIIT	α	UT a	rap	TIIT	Ω±α	vα⊥	TAT	
rne	-										_				4	
riie	-		100					105			_		110		1	

Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr

115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 130 135

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<221> CDS

<222> (1)..(351)

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<222> (1)..(24)

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gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctc tcc tgc agg 96
Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg

gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct 144
Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
35 40 45

ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act 192
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
50 55 60

ggt atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act 240 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr 65 70 75 80

ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtt tat tac tgt 288
Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
85 90 95

cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag 336 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys 100 105 110 ctg gag atc aaa cga Leu Glu Ile Lys Arg 115

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<211> 117

<212> PRT

<213> Homo sapiens

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Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
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Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro 35 40 45

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
50 55 60

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
65 70 75 80

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys 85 90 95

Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
100 105 110

Leu Glu Ile Lys Arg 115

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<212> DNA

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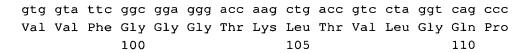
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_		_	_		_	_	gct Ala						_	_		96
_		_			_	_	gcc Ala 40								-	144
							ggt Gly									192
_		_	-	_			gcg Ala							-		240
_		_	_	_	_	_	tct Ser		_	-	_				_	288
	_	_	_	-	_		tgg Trp						_			336
-	_		gtc Val													354
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Ala	Ile	Ser 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Gln	Gly	Leu 45	Glu	Trp	Met	
Gly	Gly 50	Ile	Ile	Pro	Ile	Phe 55	Gly	Thr	Ala	Asn	Tyr 60	Ala	Gln	Lys	Phe	

Gln 65	Gly	Arg	Val	Thr	Ile 70	Thr	Ala	Asp	Glu	Ser 75	Thr	Ser	Thr	Ala	Tyr 80	
Met	Glu	Leu	Ser	Ser 85	Leu	Arg	Ser	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
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	Ser	Glu	Leu		Gln	Asp	Pro	Ala		Ser	Val	Ala	Leu	_	Gln	
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aca	gtc	agg	atc	aca	tgc	caa	gga	gac	agc	ctc	aga	agc	tat	tat	gca	96
Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	
			20					25					30			
agc	tgg	tac	caq	caq	aag	cca	gga	cag	gcc	cct	gta	ctt	gtc	atc	tat	144
-			_	_	_			Gln	_		_		-			
		35					40					45				
aat	aaa	aac	aac	caa	ccc	tca	aaa	atc	cca	gac	cga	ttc	tct	aac	tcc	192
								Ile								
	50					55					60					
agc	tca	aaa	aac	aca	act	tcc	ttα	acc	atc	act	aaa	act	cad	aca	даа	240
								Thr								
65		-			70					75	-				80	
~~+	~-~	~~+	~	+-+	.	#- e #-		.		~		5 er L	~~+			200
								tcc Ser								288
			<u>-</u>	85	- <u>, -</u>	- 1 -			90	p			~-J	95		



<210> 8

<211> 111

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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr 35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser 50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro 85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro 100 105 110